

The Gut Microbiome in Adult and Pediatric Functional Gastrointestinal Disorders**Andrea Shin, M.D., M.Sc.¹****Geoffrey A. Preidis, M.D., Ph.D.²****Robert Shulman, M.D.²****Purna Kashyap, M.B.B.S.³**

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Abbreviations: CNS=central nervous system, FC=functional constipation, FD=functional dyspepsia, FGIDs=functional gastrointestinal disorders, FODMAP= fermentable oligosaccharides, disaccharides, monosaccharides, and polyols, GABA= γ -aminobutyric acid, GF=germfree, GI=gastrointestinal, IBS=irritable bowel syndrome, IBS-C=constipation predominant IBS, IBS-D=diarrhea predominant IBS, SCFA=short chain fatty acid(s), SIBO=small intestinal bacterial overgrowth, TLR=toll-like receptor; 5-HT=5 hydroxytryptamine

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ABSTRACT

The importance of gut microbiota in gastrointestinal (GI) physiology was well described, but our ability to study gut microbial ecosystems in their entirety was limited by culture-based methods prior to the sequencing revolution. The advent of high-throughput sequencing opened new avenues, allowing us to study gut microbial communities as an aggregate, independent of our ability to culture individual microbes. Early studies focused on association of changes in gut microbiota with different disease states which was necessary to identify a potential role for microbes and generate novel hypotheses. Over the past few years the field has moved beyond associations to better understand the mechanistic implications of the microbiome in the pathophysiology of complex diseases. This movement also has resulted in a shift in our focus towards therapeutic strategies which rely on better understanding the mediators of gut microbiota-host crosstalk. It is not surprising the gut microbiome has been implicated in pathogenesis of functional gastrointestinal disorders (FGIDs) given its role in modulating physiological processes such as immune development, GI motility and secretion, epithelial barrier integrity, and brain-gut communication. In this review, we focus on the current state of knowledge and future directions in microbiome research as it pertains to FGIDs. We summarize the factors which help shape the gut microbiome in humans. We discuss data from animal models and human studies to highlight existing paradigms regarding the mechanisms underlying microbiota-mediated alterations in physiological processes and their relevance in human interventions. While translation of microbiome science is still in its infancy, the outlook is optimistic and we are advancing in the right direction towards precise mechanism based microbiota therapies.

INTRODUCTION

The human gut is home to a complex microbial ecosystem with bacteria, fungi, viruses, and archaea which exist in a mutualistic relationship with the host in homeostatic conditions. The microbial members along with their genetic content are often referred to as the gut microbiome and can be viewed as a “dynamic organ” capable of mediating a wide variety of biochemical transformations that directly impact host physiology in health and disease^{1, 2}. However, a disruption in this equilibrium can lead to alteration of host physiology resulting in disease states such as functional gastrointestinal disorders (FGIDs).

The role for gut bacteria in FGIDs such as irritable bowel syndrome (IBS) has been well described. An estimated 10% of IBS cases begin after an episode of infectious gastroenteritis³. However, the study of intestinal microbial ecosystems was limited by our inability to identify bacteria without cultivating them in the laboratory. At the turn of the century, ground-breaking advances in the genomics era and sequencing technologies^{4, 5} gave way to culture-independent molecular approaches allowing us to not only identify and characterize microbial communities based on similarities in DNA sequences, but also provide knowledge that has significantly improved our ability culture bacteria that were previously considered unculturable⁶.

These advances have led to extensive characterization of microbial communities in FGIDs over the past decade. While no consistent “microbial signature” has been associated with FGIDs, several lines of evidence support a role for gut microbes in the development of FGID symptoms⁷. There has been a significant effort to move beyond describing associations between the gut microbiome and FGIDs to defining mechanisms underlying microbial contributions to the pathophysiology of FGIDs.

In this review, as a part of our effort to define a path from bench to bedside, we will summarize factors affecting the gut microbiome and describe a conceptual framework for the role of the gut microbiome in FGIDs. This foundation will allow us to identify gaps in our current body of knowledge and develop strategies to translate microbiome science into improved diagnosis, prognosis, and management of FGIDs.

Factors that shape the gut microbiota

Gut microbial composition and diversity is largely the consequence of host selection pressures such as genetics, habits, sex, and location within the gastrointestinal (GI) tract as well as environmental factors including diet (**Figure 1**). Gut microbial diversity varies with age, and substantial differences are seen at the extremes of life⁸. At birth, assembly of the gut microbiota begins with colonization from environmental microbes (e.g., maternal vaginal, fecal, skin microbiota). In the subsequent months to years, gut microbial communities continue to shift in response to key life events (e.g., exposure to solid foods, illnesses, antibiotics) with gradual increases in diversity and convergence to an “adult-like” microbiota⁹⁻¹¹. The adult gut microbiota is relatively stable over time and surprisingly resilient to temporary perturbations, changing as we get older to a distinct and less diverse microbiome¹².

Sex associations (**Figure 1**) with the gut microbiota have been characterized by increased relative abundance of Firmicutes and lower Bacteroidetes in women compared to men and may be further influenced by body mass index^{13, 14}. Host genetic influence^{15,16,17 18, 19,20} on the gut microbiome is apparent from studies of monozygotic and dizygotic twin pairs that demonstrate shared community structures between related individuals²¹ and temporally stable heritable taxa¹⁷. However, the effect size is likely small given recent microbial-genetic association studies showing environmental factors to have substantially greater impact on the gut microbiome than

genetics²². The impact of both short²³ and long term dietary patterns²⁴ on the gut microbiome cannot be overstated^{25, 26}. The role of diet²⁷ in microbial alterations is of significant interest in FGIDs as dietary intolerances are commonly reported in FGIDs and patients may alter or restrict their diets based on perceived associations between symptoms and food^{28, 29}. The interaction of diet, gut microbiome, and symptoms in FGIDs (reviewed in ³⁰) has not been well studied and the long term consequences of current dietary interventions with reported benefit in IBS, such as supplementation with psyllium fiber and the low FODMAP (fermentable oligosaccharides, disaccharides, monosaccharides, and polyols) diet^{31, 32}, on the gut microbiome remain to be seen.

Other modifying factors (**Figure 1**) include psychological stress^{33,34}, physical activity³⁵, tobacco use³⁶, alcohol consumption³⁷, and antibiotic exposure^{38, 39,40}. In one population-level analysis of gut microbiome variation, 69 factors were shown to correlate with microbiome community variation, with stool consistency emerging as the most influential covariate⁴¹.

The distribution and composition of the gut microbiota changes along the length of the GI tract (**Figure 2**) and across the lumen, mucus layer, and the epithelium^{42, 43}. Bacterial density increases from more proximal to distal sites⁴⁴. Microbial abundance and community structure in the proximal intestine is affected by gastric acid, pancreaticobiliary secretions, and fast transit⁴⁵. Spatial niche partitioning of microbial populations can also be a result of mucus from goblet cells⁴⁶ and differential oxygen tolerance⁴⁷. Together, these factors lead to distinct microenvironments driving the biogeographical stratification of microbes across the GI tract.

EFFECT OF THE GUT MICROBIOTA ON HOST PHYSIOLOGY

Gut microbiota and gastrointestinal motility

Altered GI motility and transit have long been recognized in the pathobiology of FGIDs such as IBS⁴⁸ and functional dyspepsia (FD)^{49,50}. GI motility and the gut microbiota have reciprocal effects (reviewed in ¹), highlighting a bidirectional relationship (**Figure 3**). Gut microbes can accelerate GI transit^{51,52}. In turn, accelerated GI transit can alter the composition and spatial organization of microbial communities by creating luminal conditions suited for the growth of specific bacterial taxa or by affecting bacterial adherence¹. Interestingly, GI motility related changes in the gut microbiome can further perpetuate the alteration in GI motility as a positive feedback effect⁵³. Several microbial mediators (**Table 1**) of GI motility have been identified (**Figure 3**), including short chain fatty acids (SCFAs) and bile acids. SCFAs are produced by fermentation of dietary starches or complex carbohydrates by gut bacteria⁵⁴, while bile acid deconjugation and dehydroxylation by gut bacteria regulates the quantity and derivatives of bile acids in the colon. SCFAs and bile acids may affect gut motility (Table 1). Prokinetic effects of bile acids can be mediated by the G protein-coupled bile acid receptor TGR5 (or GPBAR1), expressed by enteric neurons and enteroendocrine cells based on findings from animal models⁵⁵. Interestingly, microbial mediators of GI motility can vary by diet^{56,57}. For example, turmeric, a commonly used spice in Asian dishes, stimulates gallbladder contraction and increases intraluminal bile acids through its active ingredient, curcumin. Similarly, SCFA concentrations can vary based on dietary carbohydrate and protein intake. Other microbial products or metabolites (**Table 1**) that have been identified as potentially relevant in microbial regulation of GI motility include: bacterial lipopolysaccharide, which can improve survival of enteric neurons by activation of toll-like receptor 4 (TLR4)⁵⁸. Preliminary studies support the roles of other microbial metabolites such as hydrogen sulfide^{59,60}, tryptamine⁶¹, and hydrogen

gas⁶² in regulation of human GI motility by their putative effects on GI smooth muscle and the enteric nervous system¹.

Gut microbiota and gastrointestinal sensation

Abdominal pain in IBS⁴⁸ and other FGIDs⁶³ such as FD⁶⁴ and functional abdominal bloating/distention⁶⁵ has been attributed to visceral hypersensitivity to mechanical and chemical stimuli. Evidence for a role of the gut microbiome in regulating GI sensation (**Figure 3**) comes from gnotobiotic studies showing transfer of the visceral hypersensitivity phenotype following transplantation of gut microbiota from patients with IBS into germ-free (GF) mice⁶⁶. A recent study by Riba et al.⁶⁷ demonstrated a correlation between visceral hypersensitivity and increase of *Escherichia coli* abundance followed by induction of hypersensitivity in response to *E. coli* gavage in mice. Disruption of the gut microbiota in early-life also has been associated with long-term changes in visceral sensitivity, emphasizing the importance of the gut microbiome in neurodevelopment of pain pathways⁶⁸. The exact mechanisms by which bacteria affect visceral perception and sensation still need to be determined. A few putative mechanisms include: microbial induction of epithelial μ -opioid and cannabinoid receptors as shown with oral administration of *Lactobacillus* strains in rodents⁶⁹; regulation of central⁷⁰ and peripheral neuronal pathways⁷¹; anti-nociceptive effects from inhibition of transient receptor potential vanilloid as shown with administration of *Lactobacillus reuteri*⁷² in rats; microbial metabolites (e.g., organic acids) or byproducts (e.g. nitric oxide)⁷³ altering sensation; and microbially-derived bioactive molecules such as γ -aminobutyric acid (GABA) as shown with administration of GABA-producing *Bifidobacterium dentium*⁷⁴. The translation of findings from animal models to humans can, however, be challenging. For instance, rectal administration of butyrate increases

colonic hypersensitivity in rats⁷⁵, but results in decreased visceral sensitivity in healthy humans⁷⁶. Hence, findings from animal studies, while valuable, need to be validated in humans.

Gut microbiota and intestinal permeability

The intestinal epithelium and the overlaying mucus layer serve a key role in protecting the host by providing a physical and immunological barrier against potentially harmful pathogens while also regulating fluid and nutrient absorption⁷⁷. Increased permeability or disruption of the epithelial barrier has been implicated in the pathophysiology of FGIDs^{78, 79}. Microbes (**Figure 3**) can directly alter expression of tight junction proteins such as claudin-3⁸⁰ and zonula occludens-1⁸¹ or enhance expression of genes involved in tight junction signaling⁸². Microbial metabolites such as bile acids^{83,84} and SCFAs can also regulate intestinal permeability (**Table 1**). The mucus layer overlaying the epithelium is a reservoir of antimicrobial peptides and immunoglobulins and provides the first line of defense against gut bacteria⁸⁵. The mucus layer is compositionally rich in polysaccharides which can serve as a nutrient source for subsets of bacteria. Hence microbial starvation such as with decreased consumption of fiber can increase microbial reliance on the mucus polysaccharides resulting in degradation of the mucus layer and increasing susceptibility to opportunistic pathogens and inflammation^{27, 86}.

Gut microbiota, immune activation, and inflammation

Inflammation or immune activation involving both the innate and adaptive immune systems has been described in subsets of patients with FGIDs^{87,88}. There are several lines of evidence in support of the activation of mucosal and systemic immune responses by gut microbiota (**Figure 3**). Post-infectious FD is associated with increased numbers of duodenal CD68+ cells and eosinophils when compared with other subtypes of FD (epigastric pain

syndrome, post-prandial distress syndrome), and healthy states⁸⁹. Increased expression of pro-inflammatory cytokines may be elicited through interactions between bacterial components and pattern recognition receptors including TLRs such as TLR2 and TLR4 that have been associated with IBS⁹⁰. The gut microbiota can also influence immune activation via effects on lineage differentiation of T-cell subsets⁹¹, host-receptor mediated signaling as seen with *L. reuteri* activation of histamine H2 receptor signaling⁹², and production of microbial metabolites (**Table 1**).

Gut microbiota and intestinal secretion

Changes in small intestinal⁹³ and colonic secretion represents another pathophysiologic disturbance in FGIDs that may be influenced by the gut microbiome⁴⁸ (**Figure 3**). Secretory mechanisms are common therapeutic targets^{94, 95} of medications used to treat FGIDs. Microbial mediators of altered intestinal secretion⁹⁶ include metabolites from breakdown of dietary polysaccharides as well as bile acids (**Table 1**). Specific bile acids, such as deoxycholate and chenodeoxycholate, can stimulate intestinal chloride secretion^{97, 98} which is accompanied by water. SCFAs, like bile acids, are important intraluminal determinants of mucus and water secretion through effects on sodium and water influx⁹⁹, duodenal bicarbonate secretion¹⁰⁰, and colonic epithelial 5-HT₃ receptor expression¹⁰¹.

Gut microbiota and gastric function

Disturbances in gastric motor and sensory function, including impaired gastric accommodation and increased intragastric pressure, may underlie FGIDs and are often related to food intake¹⁰². There is a paucity of data in support of microbial regulation of gastric function. The administration of the prebiotic arabinoxylooligosaccharide in healthy volunteers was not

associated with changes in gastric sensitivity, compliance, or accommodation despite increased colonic fermentation¹⁰². Reported associations between the presence of small intestinal bacterial overgrowth (SIBO) and delayed gastric emptying¹⁰³ have not discerned whether associations are a result of microbial mechanisms or merely representative of underlying impairment in small intestinal motility and other confounding factors including chronic acid suppression and opioid analgesics¹⁰⁴. Recent evidence showing a similar gastric emptying time among patients with and without SIBO suggests that bacterial overgrowth does not necessarily predispose to impaired gastric emptying^{105, 106}.

Gut microbiota and central nervous system function

The bidirectional microbiome-gut-brain axis (**Figure 3**) represents the reciprocal regulation of the gut microbiome and the central nervous system (CNS). Recent studies highlight the role of the gut microbiome in modulating brain-gut communication, which may significantly affect the pathophysiology of symptoms associated with FGIDs^{107,108}. Signals from the CNS can influence GI physiology while simultaneously shaping the gut microbial fingerprint as seen in early life stress rodent models which exhibit alterations in gut microbial community composition¹⁰⁹. Similar findings have been described in other rodent stress models³³. Conversely, microbial colonization and community composition are critical to development of the hypothalamus–pituitary–adrenal axis as evidenced by the exaggerated adrenocorticotrophic hormone and corticosterone release in germ-free (GF) mice. This exaggeration is attenuated following colonization with *Bifidobacterium infantis*¹¹⁰. A different strain within the same genus, *Bifidobacterium longum* NCC3001, decreases anxiety-like behavior in mice through vagally mediated pathways¹¹¹. Microbial metabolites such as SCFAs and microbially-derived

neurotransmitters such as GABA and 5-HT may further impact brain function and mental health¹⁰⁸.

FUNCTIONAL GI DISORDERS

Role of gut microbiota in pathophysiology of irritable bowel syndrome

The gut microbiota of patients with IBS is an area of considerable interest, and has been the most extensively studied among the various FGIDs (reviewed in ⁴⁴). Despite the lack of a uniform “IBS-microbiota” pattern, key observations include a decrease in α -diversity and alterations in relative abundance of specific taxonomic groups including an increased ratio of Firmicutes to Bacteroidetes, decreased *Lactobacillus* and *Bifidobacterium*, and increased *Streptococcus* and *Ruminococcus* spp.¹¹². Cross-sectional analysis of extensively phenotyped cohorts also has revealed that while stool consistency is a significant contributor to gut microbiome compositional variation, the contribution imparted by IBS was much less⁴¹. These data highlight the importance of investigating specific pathophysiologic disturbances, beyond merely providing descriptive analyses of a heterogeneous patient populations in elucidating the role of the gut microbiome in IBS. Correlative associations between the gut microbiome and IBS have been followed by efforts to better characterize the mechanistic link between the microbiome and pathophysiology of symptoms associated with IBS (**Table 2**). Among the various aforementioned aspects of gut physiology that are affected by the gut microbiome, many are directly implicated in the pathophysiology of IBS.

Summary of findings from animal studies

Animal models, although imperfect correlates to IBS pathophysiology in humans, have allowed us to explore putative interactions between the gut microbiome and mechanisms

implicated in IBS such as altered motility, visceral hypersensitivity, increased permeability, immune activation, intestinal secretion, and disturbances in central mechanisms. De Palma et al.⁵² recently demonstrated that GF mice colonized with the fecal microbiota of diarrhea-predominant IBS (IBS-D) patients exhibited faster GI transit, increased colonic permeability, increased anxiety-like behavior, and increased infiltration by CD3⁺ T lymphocytes compared to those colonized by microbiota from healthy controls. Study of specific IBS pathways include reports describing microbiota-induced hypersensitivity to colonic distension in GF rats inoculated with the fecal microbiota from IBS patients⁶⁶. Microbial regulation of host immune responses may be further relevant to IBS. An increase in mucosal immune cells including mast cells, macrophages or monocytes, T-cells, and eosinophils has been reported in both pediatric and adult FGID populations^{79, 113, 114}. Mast cells contain biologically active substances including histamine, tryptase, cytokines, and membrane-derived arachidonic acid metabolites (e.g., prostaglandins) that are released upon their activation. These mediators may alter nociceptive pathways in IBS¹¹⁵ or increase intestinal permeability¹¹⁶. Macrophages and monocytes are important in modulating the adaptive immune responses and producing proinflammatory cytokines such as IL-6 and IL-8 which in some studies are increased in IBS patients¹¹⁷. The role of gut microbes in these immune pathways remains unknown.

Summary of findings from studies in adult IBS patients

Numerous studies have examined microbiome-related effects on pathophysiological changes in IBS, building upon work performed in animal models. Interventional studies investigating the use of probiotic and antibiotic therapy in IBS have led to identification of potential microbial effects on transit (**Table 2**). Treatment with a probiotic containing *Bifidobacterium lactis*¹¹⁸ accelerates whole gut transit and improves symptoms in patients with

constipation-predominant IBS (IBS-C), while treatment with the non-absorbable antibiotic rifaximin is associated with increases in both ascending colonic emptying and overall colonic transit rate at 48 hours¹¹⁹ in non-constipated IBS patients. A role for the gut microbiome in immune modulation was suggested by findings from the clinical trial wherein *B. infantis* 35624 alleviated symptoms and was associated with normalization of abnormal IL-10/IL-12 ratios in IBS patients¹²⁰. Colonic mucosal gene expression profiling of IBS patients also has found differential expression of genes associated with host immune responses against microbial invasion, further suggesting that immune activation may be shaped by microbial interactions¹²¹. Alterations in mucus-associated bacteria that may influence mucus integrity and intestinal secretion (e.g. *Akkermansia muciniphila*, *Ruminococcus gnavus* and *Ruminococcus torques*) also have been associated with IBS¹²². Microbially-mediated effects on intestinal secretion in IBS may be a consequence of differential bile acid biotransformation by the gut microbiome⁹⁶. This concept is supported by the decreased concentrations of fecal unconjugated bile acids known to stimulate colonic secretion (deoxycholate and chenodeoxycholate) in IBS-C¹²³. Regarding the role of the microbiome-gut-brain axis in IBS (reviewed in ¹²⁴ and ¹²⁵), probiotic therapy has been shown to modulate CNS function in healthy volunteers¹²⁶ through effects on brain regions controlling processing of emotion and sensation. More recently, in a recent placebo controlled trial in IBS patients, treatment with the probiotic *B. longum* NCC3001 was associated with improved symptoms of depression and changes in brain activation patterns measured by functional magnetic resonance imaging¹²⁷.

Summary of findings from studies in pediatric IBS patients

Similar to adult studies, the composition of the gut microbiome differs between children with IBS and age-matched healthy controls, despite lack of a uniform “IBS-microbiota”

signature across studies. One study enrolling children ages 7-12 years found pediatric IBS to be associated with decreased relative abundance of *Bacteroides* spp. and increased relative abundance of the class Gammaproteobacteria, including *Haemophilus parainfluenzae*, along with increased abundance of novel taxa related to the genus *Ruminococcus*. In this cohort, microbiota composition correlated with abdominal pain severity and frequency, and could be used to distinguish IBS-C from unsubtyped IBS¹²⁸. Another study of children ages 11-18 years found IBS-D to be associated with increased abundance of the genera *Veillonella*, *Prevotella*, *Lactobacillus*, and *Parasporobacterium*, and with decreased abundance of *Bifidobacterium* and *Verrucomicrobium*¹²⁹. By adding fecal metabolomic profiling to microbiome signatures, stool from children with IBS-D could be more accurately discriminated from that of healthy controls, with formate, pyruvate, and glucose being the most predictive metabolites¹³⁰. Fecal microbial community composition also might be used to predict which children with IBS are more likely to respond to a low-FODMAP diet: in two separate studies, responders had distinct baseline microbiome signatures compared to non-responders^{131, 132}.

Among the most studied probiotics in pediatric IBS is *Lactobacillus rhamnosus* GG, which was found in a meta-analysis of three randomized, placebo-controlled trials (RCTs) to confer a modest but significantly increased rate of treatment response versus placebo¹³³. Two multicenter, randomized, double-blind, placebo-controlled crossover studies provide further evidence of microbiota involvement in pediatric IBS. One study found that VSL#3 improved GI symptoms¹³⁴, while the other reported that a combination of three bifidobacteria resolved abdominal pain and improved quality of life to a greater extent than placebo¹³⁵. On the other hand, psyllium fiber reduced pain episodes in an RCT enrolling children with IBS without altering the composition of the gut microbiota based on 16S ribosomal RNA analysis¹³⁶.

RCTs in children with functional abdominal pain (FAP) have revealed that *L. reuteri* DSM 17938 is effective in treating abdominal symptoms. Jadrešin et al.¹³⁷ demonstrated a reduction in days with pain and pain severity in children with IBS and FAP. In studies focused specifically on FAP, Romano et al.¹³⁸ reported reduced pain severity and Weizman et al.¹³⁹ and Maragkoudaki et al.¹⁴⁰ both reported reduced pain severity and frequency in those treated with the probiotic compared with placebo.

In summary, both animal and human studies underscore the importance of the gut microbiome in mediating peripheral and central mechanisms implicated in IBS. Moreover, factors affecting gut microbiota composition are akin to the etiological factors in IBS and probiotic interventions have a generally beneficial effect. However, given the heterogeneous nature of the disease with multiple putative mechanisms, our broad nontargeted approach without consideration for the underlying physiological disturbance likely dilutes the overall impact and makes it difficult to ascertain the precise benefit of microbiota modulation. As we move forward, it will be important to phenotype patients based on the underlying physiological alterations so that we can develop targeted approaches directed towards specific microbes driving the host phenotype.

Role of gut microbiota in pathophysiology of functional dyspepsia

Similar to IBS, multiple pathogenic mechanisms including altered gastric function, visceral hypersensitivity, low grade inflammation or immune activation, increased duodenal permeability, and abnormal CNS function have been postulated to contribute to symptoms in FD¹⁴¹. As summarized above, gut microbiota have been shown to modulate the majority of these physiological functions. Although data on the gastroduodenal microbiome and its particular role

in FD are sparse, there are a few studies that lay the groundwork for future work investigating the role of microbial community alterations in FD.

Summary of findings from animal studies

In general, animal studies investigating microbial effects on putative pathophysiologic mechanisms in FD are lacking given the absence of reliable models. The described effects are attributed to fermentative end products such as SCFAs. Bacterially-derived or ingested SCFAs can alter duodenal bicarbonate secretion¹⁰⁰. In addition, the absorption of SCFAs can also influence the luminal bacterial population which may be relevant in FD¹⁰⁰.

Summary of findings from studies in adult patients with functional dyspepsia

There are few human studies describing the gut microbiome in patients with FD, hence the precise role of the microbiota remains unknown. SIBO has been proposed to trigger symptoms in FD¹⁴², although studies examining the role of SIBO in FD are limited by the relative inaccessibility of the more distal regions of the small intestine and concerns regarding accuracy and interpretation of available testing methods for the diagnosis of SIBO¹⁴³. Recently, Zhong et al.¹⁴⁴ found the relative abundance of the anaerobic genera *Prevotella*, *Veillonella* and *Actinomyces* were significantly decreased in the duodenal mucosa of nine patients with FD compared to controls. Interestingly, severity of symptom responses to a standardized meal was positively correlated with mucosal bacterial load, which in turn was inversely correlated with bacterial diversity. Igarashi et al.¹⁴⁵ found that gastric fluid samples from patients with FD were characterized by an increased Bacteroidetes to Proteobacteria ratio and absence of Acidobacteria. In contrast, healthy volunteers had a decreased Bacteroidetes to Proteobacteria ratio and presence of Acidobacteria. Non-blinded probiotic therapy with *Lactobacillus gasseri* OLL2716 was

subsequently associated with shifts in gastric fluid microbial community composition similar to that found in healthy controls. In another RCT among patients with FD, rifaximin treatment was associated with significant improvement in global dyspeptic symptoms, belching, and post-prandial fullness/bloating, further suggesting a potential role for the microbiome in FD¹⁴⁶.

Summary of findings from studies in pediatric patients with functional dyspepsia

Relatively little is known regarding the gut microbiome in pediatric FD. Although the previously highlighted multicenter, randomized, double blind, placebo controlled crossover study reported that a combination of three probiotic bifidobacteria improved pain scores and quality of life among 48 children with IBS, no benefit was observed among the 25 enrolled children who had FD, perhaps owing to the small number of patients treated¹³⁵. Likewise, the moderate overall benefit associated with *L. rhamnosus* GG treatment in an RCT of children with IBS or FD was not observed in the subset of children with FD¹⁴⁷. However, it would be premature to make definitive conclusions given the small sample size (n=20 with FD versus n=37 with IBS).

In summary, the gut microbiome can affect mechanisms underlying FD similar to IBS, but the microbial community composition of the stomach and small bowel remain elusive and much work is needed before we can target specific microbial mediators that drive symptoms in FD. The overall positive impact of probiotics is encouraging and highlights the need for better mechanistic understanding in order to develop more precise microbiota-based therapeutics.

Role of gut microbiota in pathophysiology of functional abdominal bloating

Abdominal bloating and distension are common complaints among patients suffering from FGIDs, and are among the most challenging symptoms to treat. The pathophysiologic mechanisms contributing to bloating are poorly understood, although SIBO and alterations in gut

microbial communities have been hypothesized¹⁴⁸ to play a role through microbial fermentation of dietary nutrients. As this is predominantly a subjective sensation, there are no animal models to mimic these symptoms.

Summary of findings from adult patients with functional abdominal bloating

The majority of clinical studies investigating symptoms of bloating have been performed in IBS patients, with bloating and distension evaluated as secondary endpoints¹⁴⁸. A recent study showed depletion of operational taxonomic units within *Subdoligranulum* and *Anaerovorax*, belonging to the families Ruminococcaceae and Eubacteriaceae, respectively, in IBS patients without bloating compared to those with bloating and to healthy controls¹⁴⁹. Placebo-controlled studies of antibiotic (rifaximin) treatment in FGIDs and IBS have demonstrated significant reduction in bloating scores with rifaximin compared to placebo¹⁵⁰⁻¹⁵². Efficacy of probiotic administration for symptoms of bloating have been less consistently reported¹⁵³ although some studies in IBS patients have suggested benefit with specific probiotic strains including *B. lactis* DN-173¹¹⁸, *Bifidobacterium animalis* DN-173 010¹⁵⁴, and VSL#3¹⁵⁵.

Summary of findings from pediatric studies

Little is known regarding the microbiome in functional abdominal bloating in children. The trial noted previously by Weizman and colleagues¹³⁹, which reported benefit for abdominal pain with the probiotic *L. reuteri* DSM 17938, also reported a lower incidence of perceived abdominal distention and bloating. Similarly, patients in the VSL#3 trial had decreased abdominal bloating/gassiness compared to placebo¹³⁴.

In summary, while gut microbes can potentially impact these symptoms both via fermentative end products and by their effect on visceral sensation, we need to better characterize the potential microbial mediators in order to develop relevant therapeutics.

Role of gut microbiota in pathophysiology of functional constipation

There is evidence supporting an association between the altered mucosal and fecal microbiota and chronic constipation^{156, 157}. Most of our knowledge regarding the effects of the gut microbiota on peripheral mechanisms associated with constipation, such as GI motility, comes from animal studies. However, in recent years, several studies have been published exploring the gut microbiome in patients with constipation (**Table 2**).

Summary of findings from animal studies

Investigation of the causal relationship between alterations in gut microbial communities and constipation has been described in a recent study¹⁵⁸ reporting upregulation of 5-HT transporter and decreased 5-HT content in the colonic tissue of germ-free mice that received fecal microbiota from constipated patients. 5-HT was negatively correlated with transit time and changes were accompanied by decreased relative abundance of the phylum Firmicutes and increased Bacteroidetes in mice receiving fecal microbiota from constipated patients. Genus level analyses further showed decreased relative abundance of *Clostridium*, *Lactobacillus*, *Desulfovibrio* and *Methylobacterium* and increased relative abundance of *Bacteroides* and *Akkermansia*. The findings suggest a potential role for gut microbiota in the pathogenesis of chronic constipation via increased expression of 5-HT transporter¹⁵⁸. Interestingly, gut microbiota changes resulting from constipation can further impact GI motility, suggesting a more complex interaction with feedforward regulation rather than a simple cause-effect relationship⁵³.

The potential role of microbially-derived metabolites is further supported by findings of delayed GI transit and altered SCFA and bile acid profiles following transfer of fecal microbiota from patients with slow transit constipation to antibiotic-treated mice¹⁵⁹.

Summary of findings from adult patients with functional constipation

Several studies have reported a positive relationship between prolonged colon transit times, with increased richness and diversity of the fecal microbiome in adults without prior history of GI disorders^{160,161}. However, the association between constipation and the gut microbiome may involve mechanisms beyond that of slow transit. In a study of adults with chronic constipation, overall composition of the colonic mucosa-associated microbiota could discriminate patients with constipation from control subjects independent of transit time¹⁵⁷. Taxonomic profiling of the fecal microbiome from patients with functional constipation (FC) and healthy volunteers has shown decreased abundance of *Bacteroides*, *Roseburia*, and *Coprococcus* in FC patients. Furthermore, healthy volunteers were found to have a gut microbiome enriched in genes involved in carbohydrate, fatty acid, and lipid metabolism while FC patients harbored a high abundance of genes involved in methanogenic pathways, hydrogen production, and glycerol¹⁶². Analysis of functional gene targets in constipated and healthy females also has demonstrated increased abundance of hydrogenogenic (hydrogen producing) and hydrogenotrophic (hydrogen utilizing) genes by qPCR in colonic mucosa of constipated individuals¹⁶³.

Summary of findings from pediatric studies

In a cross-sectional study of 8 constipated obese children and 14 non-constipated obese children, FC was associated with decreased abundance of the phylum Bacteroidetes, including a

significant reduction of the genus *Prevotella*, and increased abundance of multiple genera within the phylum Firmicutes, including *Blautia*, *Coprococcus*, and *Ruminococcus*¹⁶⁴. A recent systematic review included seven RCTs enrolling a total of 515 children that investigated the effects of probiotics in pediatric FC. Although two of the included studies, those evaluating *L. reuteri* DSM 17938¹⁶⁵ and *B. longum*¹⁶⁶, reported significantly increased defecation frequency in the treatment arm, the meta-analysis concluded that there is currently insufficient evidence to support the use of probiotics for pediatric FC¹⁶⁷. Finally, although a low-fiber diet is a known risk factor for FC in children¹⁶⁸, there is currently little evidence to support the use of fiber for pediatric FC. Multiple systematic reviews note the sparse data and high risk of bias among the current evidence base¹⁶⁹⁻¹⁷².

In summary, the reciprocal interactions between GI transit and gut microbiota suggest that even if changes in gut microbiota are initiated by a change in transit, the altered microbial community can perpetuate the alteration in GI transit, highlighting the adaptability of the gut microbial community. Consequently, we need to think beyond the simple cause-effect paradigm as irrespective of the inciting event that alters the microbial community, these changes can still perpetuate a disease phenotype. The effect of gut microbiota on the host serotonergic system provides a plausible target for altering GI transit.

Role of gut microbiota in pathophysiology of infant colic

Infant colic, a characteristic group of behaviors featuring prolonged crying, is present in up to 25% of infants at 6 weeks of life¹⁷³ and is associated with increased risk of recurrent abdominal pain and allergic disorders later in childhood¹⁷⁴. Underlying mechanisms are unclear, due in part to a lack of small animal models. Multiple pathophysiologies, including gut microbiome alterations, have been proposed to promote abdominal pain. Early culture-dependent

studies by Savino et al. revealed that colicky infants were more frequently colonized by anaerobic gram-negative proinflammatory bacteria and less frequently colonized by lactobacilli when compared to non-colicky infants^{175, 176}. Subsequent molecular studies confirmed enrichment of proinflammatory and gas producing taxa within Proteobacteria in stool from colicky infants¹⁷⁷⁻¹⁷⁹.

Given these observations, the probiotic *L. reuteri*, one of the few endogenous lactobacilli in the human GI tract, was proposed as a means of normalizing these gut microbial community alterations and potentially reducing crying times in infant colic and has become the most extensively studied microbiome-targeting therapy for colic. *L. reuteri* has been tested in six prospective, RCTs: two meta-analyses that included more than 400 infants found that *L. reuteri* significantly reduced crying time in formula fed infants by a mean of nearly one hour per day^{180, 181}. Of note, the only other therapy to demonstrate efficacy in infant colic was fennel oil while often-recommended interventions including simethicone and maternal diet manipulation produced mixed results¹⁸¹. Interestingly, *L. reuteri* also has shown benefit in prevention trials, reducing the risk of developing colic at three months of life^{182, 183}. Finally, a number of small studies have tested other microbiome-targeting therapies, including *L. rhamnosus* GG^{184, 185} and a synbiotic combination of fructooligosaccharide and seven probiotics¹⁸⁶; these small studies generated mixed results.

Modulating the gut microbiota for treatment of functional gastrointestinal disorders

Targeting the gut microbiota for therapeutic intervention in FGIDs remains an area of significant interest for patients and clinicians. Probiotics have been studied extensively in adult and pediatric FGID populations as previously discussed and summarized in Table 2. A prior systematic review of probiotics in IBS suggested evidence for efficacy on global IBS symptoms,

abdominal pain, bloating, and flatulence¹⁸⁷; however, there remain many unanswered questions regarding strain-specific effects, mechanisms of action, mode of administration and dosing, and patient selection. Despite their relative accessibility and general safety, clinical recommendations regarding specific probiotic use in FGIDs are limited by a lack of rigorous clinical trial data. Rifaximin has been studied in functional dyspepsia¹⁴⁶, abdominal bloating, and flatulence¹⁵⁰, and is approved for treatment of adults with IBS-D¹⁵¹. The exact mechanisms by which rifaximin exerts its effects in IBS, however, remain uncertain, with a recent study of patients with non-constipated IBS showing borderline effects on microbial richness and increased rates of proximal colonic emptying but no clear effects on bowel function, permeability, or production of intraluminal metabolites¹¹⁹. More recently, results of several trials investigating the efficacy of fecal microbiota transplantation (FMT) for IBS have been reported. In one RCT among patients with moderate-to-severe IBS, higher response ($p=0.049$) rates at three months, defined as a 75-point improvement in the IBS severity scoring system, were observed in patients receiving FMT (65%) compared to those receiving placebo (43%). However, differences were no longer significant at 12 months followup¹⁸⁸. On the other hand, a separate multicenter RCT¹⁸⁹ comparing FMT capsules to placebo in patients with diarrhea-predominant IBS was unable to demonstrate significant symptom relief at three months with FMT, although subgroup analysis suggested patients with post-infectious IBS experienced greater improvement with FMT compared to placebo ($p=0.09$). The role of FMT in IBS needs to be better defined as there may be specific features in the donor microbiome as well as additional recipient characteristics that predict clinical outcomes. FMT, however, represents a stop-gap measure and it is imperative that we determine which specific microbes, microbial consortia, or microbial products yield benefit in FGIDs to provide precision care without unwanted effects.

TRANSLATING MICROBIOME RESEARCH: Where are we, and what do we need?

The role of the gut microbiome in FGIDs must be considered in the context of the environment, the host, and host-specific factors. In order for us to advance the field and develop novel microbiota-based diagnostic and therapeutic targets in FGIDs, we will need to move from simple taxonomic associations to functional phenotypes and mechanism-based studies. In animal studies, we need to determine the specific microbes or microbial products as well as the mechanisms that alter host physiology. The use of gnotobiotic models allows inclusion of heterogeneity among gut microbiome and diet similar to human subjects, phenotype transfer to better understand cause-effect relationships, and complex reciprocal interactions among the host and microbiome. In terms of human studies, we need well controlled longitudinal studies incorporating functional genomic, transcriptomic, metagenomic, and metabolomic analyses as well as robust clinical metadata for the evaluation of “mechanism-based phenotypes.”. There are several factors that can affect the gut microbiome including diet, demographics, body mass index, medication etc. as described above and hence these should be controlled before linking the microbiome with host outcomes. In addition to understanding the role of microbiome in the pathophysiology of symptoms in FGIDs, assessing the impact of the microbiome on efficacy of dietary and pharmacologic therapy in conjunction with host features will allow for better treatment stratification compared to the current one size fits all approach. Finally, we need to move the needle from empirically selected prebiotic and probiotic therapies to the next generation of precise mechanism-based diagnostic and therapeutic interventions. The use of genetically engineered bacterial strains to assess the gut environment, release metabolites of interest at specific locations within the GI tract, and optimize drug metabolism appears to be on

the horizon^{190, 191}. Rapid advances in these areas provide an optimistic outlook for microbiota-based interventions in FGIDs.

PERSPECTIVE

It is now apparent that the gut microbiome is an integral player in the pathophysiology of FGIDs through its effects on host physiological processes even though the precise mechanisms underlying microbial regulation remain an area of active investigation. The improved understanding of factors that shape the gut microbiome allow us to better identify confounding effects in human studies, including physiological development through childhood and adolescence to adulthood^{30, 12811}, and at the same time, appreciate the adaptation of this resilient microbial ecosystem to short- and long-term perturbations in host environment. A comprehensive view of the gut microbiome in both pediatric and adult FGIDs is important in order to account for the dynamics of the gut microbiome as it exhibits a continuum across the lifespan, with hallmark characteristics in different phases of life¹⁹².

The expanding ecosystem of microbiome-based startups and industry funding, the shift away from compositional changes towards functional products of the microbiome, better integration of clinical metadata, and genetic engineering and synthetic biology tools to make designer probiotics targeting specific host functions, together instill confidence in our ability to move microbiome science from bench to the bedside.

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Table 1: Microbial metabolites as mediators of gastrointestinal physiology

*SCFA=short chain fatty acid; #5-HT=serotonin; Irritable bowel syndrome; §CDCA=chenodeoxycholic acid; ^DCA=deoxycholic acid

Metabolite	Microbial regulation	Effect	Mechanism
*SCFA	Fermentation of dietary starches to SCFA	Motility	Butyrate and acetate increase #5-HT biosynthesis ¹⁹³ SCFAs provoke proximal colonic contractions via 5-HT in rats ¹⁹⁴
		Sensation	Butyrate increases colonic hypersensitivity in rats ⁷⁵ , decreases visceral sensitivity in healthy humans ⁷⁶
		Permeability	Butyrate role in maintenance of intestinal barrier ¹⁹⁵ may vary depending on local concentrations, pH, and cellular differentiation
		Immune activation	SCFAs and n-butyrate regulate neutrophil function, increased tight junction protein expression, reduce cytokine and chemokine release ¹⁹⁶
		Secretion	SCFAs promote fluid and electrolyte absorption within the gut ⁹⁹ Acetate effects both small intestine and colon through increased duodenal bicarbonate secretion ¹⁰⁰ and effects on colonic epithelial 5-HT ₃ receptor expression ¹⁰¹
Bile acids	Deconjugation and dehydroxylation	Motility	§CDCA promotes propagating and non-propagating colonic contractions in humans ¹⁹⁷ ^DCA-induced intestinal peristalsis and contractions mediated by TGR5 ⁵⁵
		Permeability	Increased permeability associated with bile acids with two hydroxyl groups in α configuration ¹⁹⁸ Bile acid receptor, TGR5, modulates intestinal barrier function in mice ¹⁹⁹
		Secretion	DCA and CDCA stimulate chloride and water secretion via inhibition of Cl ⁻ /OH ⁻ exchange (Alrefai 2007) and activation of CFTR via cAMP ⁹⁸
		Immune activation	CDCA regulates intestinal antimicrobial environment in mice via Paneth cell α -defensins and C-type lectins ²⁰⁰

Methane	Gaseous by-product	Motility	Methane augments small bowel contractility and slows intestinal transit ¹⁵²
Hydrogen sulfide	Gaseous by-product	Motility	Sulfate-reducing bacteria slow intestinal transit in mice ⁶⁰
Hydrogen gas	Gaseous by-product	Motility	Hydrogen gas shortens transit in guinea pig colon ⁶²

Table 2: Summary of studies investigating pathophysiologic mechanisms and gut microbiota in patients with functional gastrointestinal disorders

*IBS=Irritable bowel syndrome (IBS-D=diarrhea-predominant IBS, IBS-C=constipation-predominant IBS, PI-IBS=post-infectious IBS);
[&]pcbo=Placebo; +HV=Healthy volunteer; **GBA=Gut brain axis; [#]HADS=Hospital Anxiety and Depression Scale; ^ΔSCFA=short chain fatty acid; [@]LFSD= Low fermentable substrate diet; [^]scFOS= Short-chain fructooligosaccharide; ^δTFF3= urine trefoil factor 3;
[§]SBI=Serum-derived bovine immunoglobulin/protein isolate; ¹LC-DG=*Lactobacillus casei* DG; [¶]LPS=lipopolysaccharide;
[∞]BL=*Bifidobacterium longum* NCC3001

Study	Study population	Intervention	Sample	Mechanism studied	Role of microbiota
Shin et al. 2018 ²⁰¹	60 IBS*-D	<i>L. gasseri</i> BNR17 vs. pcbo ^{&}	Fecal	Transit	Transit significantly ↑ during 8 weeks with <i>L. gasseri</i> BNR17
Tap et al. 2017 ⁷	110 IBS, 39 HV ⁺	NA	Fecal, mucosal	Transit, GBA ^{**}	↑Transit with Clostridiales vs. <i>Prevotella</i> and <i>Bacteroides</i> enterotypes. No association between HADS [#] and enterotype
Acosta et al. 2016 ¹¹⁹	24 non-constipated IBS	Rifaximin vs. pcbo	Fecal	Transit, permeability, SCFA ^Δ and bile acid production	No significant effects of rifaximin on permeability, bile acids, SCFAs. Rifaximin associated with ↑ascending colon emptying, and colonic transit at 48H
Dior et al. 2016 ²⁰²	15 HV, 15 IBS-C, 16 IBS-D	NA	Fecal	Fecal bile acids	↓bacterial deconjugation of bile acids in IBS-D and IBS-C feces vs. HV
Le Neve et al. 2016 ²⁰³	100 IBS	NA	Fecal	Sensation, transit	Response to lactulose challenge associated with rectal sensitivity but not with fecal microbiota or transit
Chumpitazi et al. 2014 ¹³¹	12 IBS children	LFSD [@]	Fecal	Transit, metabolite composition	LFSD response associated with ↑abundance of <i>Sporobacter</i> and <i>Subdoligranulum</i> and ↓ <i>Bacteroides</i> , but not with transit. Stool metabolites (L-urobilin, cholate) associated with response and microbiome composition
Jeffery et al. 2012 ¹⁵⁶	37 IBS, 20 HV	NA	Fecal	Sensation, transit, GBA	Proteobacteria associated with ↑mental component and pain threshold; Actinomycetales inversely associated with depression. Desulfohalobiaceae and Methanobacteriaceae associated with transit
Labus et al. 2017 ²⁰⁴	29 IBS, 23 HV	NA	Fecal	GBA	No correlations between anxiety or depression symptom scores and microbial parameters; Clostridia and Bacteroidia correlated with

					sensory integration regions
Liu et al. 2016 ²⁰⁵	40 IBS, 15 Depression, 25 IBS and Depression, 20 HV	NA	Fecal	GBA, immune	↑Bacteroidetes and ↓Firmicutes in IBS-D, depression, and IBS-D with depression; Colonic mucosa inflammation associated with ↑ <i>Bacteroides</i> or <i>Prevotella</i>
Azpiroz et al. 2017 ²⁰⁶	79 IBS	scFOS [^] vs. pcbo	Fecal	GBA, sensation	scFOS reduced anxiety scores and increased fecal Bifidobacteria; No significant difference in rectal sensory threshold for scFOS vs. pcbo
Le Gall et al. 2011 ²⁰⁷	10 IBS, 13 UC, 22 HV	NA	Fecal	Fecal metabolites	Correlation between gut microbiota profile and metabolite composition
Heitkemper et al. 2018 ²⁰⁸	93 IBS	NA	Fecal	Permeability	Higher stool ^o TFF3 associated with lower permeability and microbial diversity. <i>Christensenellaceae</i> inversely related to stool TFF3.
Bednarska et al. 2017 ²⁰⁹	32 IBS, 15 HV	NA	Mucosal	Immune, Permeability	Increased permeability to <i>E. coli</i> strain HS and <i>S. typhimurium</i> in IBS biopsies vs. controls; ↑plasma VIP in IBS vs. HV; ↑tryptase and mast cells in IBS biopsies vs. HV
Valentin et al. 2017 ²¹⁰	15 IBS-D	SBI [§]	Duodenal brushing, fecal	Immune, permeability, metabolism	Bile acid synthesis, tryptophan metabolism, permeability and stool microbiome not significantly different with SBI. Changes in β diversity analysis, increased ↑ <i>Proteobacteria</i> <i>Burkholderiales</i> , <i>Firmicutes</i> <i>Catonella</i> , and unclassified genus organisms with SBI in duodenal microbiome.
Ko et al. 2013 ²¹¹	53 IBS-D	Herbal (GJS), Probiotic (DuoLac7S), pcbo	Fecal	Permeability	GJS with DuoLac7 ↑ <i>B. lactis</i> , <i>L. rhamnosus</i> , <i>L. plantarum</i> . No significant difference observed in permeability
Crouzet et al. 2013 ⁶⁶	3 IBS-C, 2 HV	NA	Fecal	Rectal sensitivity	IBS with rectal hypersensitivity have ↓bifidobacteria, ↑Enterobacteriaceae, and ↑H2-utilizing sulfide-producing bacteria vs. HV
Shulman et al. 2017 ¹³⁶	103 IBS children	Fiber vs. placebo	Fecal	GBA, permeability	No differences in psychological symptoms, permeability, or microbiome between groups
Compare et al. 2017 ²¹²	10 IBS-D, 10 HV (ex vivo)	LC-DG [†] , postbiotic	Mucosal	Immune	↑IL-1α, IL-6 and IL-8 mRNA, TLR-4 protein expression with ↓IL-10 mRNA levels in PI-IBS D vs. HV. LC-DG and PB ↓mRNA levels of pro-inflammatory cytokines and TLR-4 but ↑IL-10 after LPS ^{§§} stimulation

Hustoft et al. 2017 ²¹³	20 IBS-D or IBS-M	low FODMAP diet, FOS vs. pcbo	Fecal	Immune, SCFA	↓IL-6 and IL-8, fecal bacteria (<i>Actinobacteria</i> , <i>Bifidobacterium</i> , <i>Faecalibacterium prausnitzii</i>), total SCFAs, and n-butyric acid on LFD. FOS supplement then ↑levels of these bacteria, but cytokines and SCFAs unchanged.
McIntosh et al. 2017 ²¹⁴	37 IBS	low vs. high FODMAP	Fecal	Urinary metabolites	Significant correlations between relative bacterial abundance and symptoms and urinary metabolites (histamine, p-hydroxybenzoic acid)
Sundin et al. 2015 ²¹⁵	11 PI-IBS, 10 HV (ex vivo)	NA	Mucosal	Immune	IL-1β ↑ in PI-IBS vs. HV after stimulation with <i>Subdoligranulum variabile</i> ; IL-10 ↓ in HV vs. PI-IBS after stimulation with <i>Eubacterium limosum</i> .
Sundin et al. 2015 ²¹⁶	13 PI-IBS, 19 IBS, 16 HV	NA	Fecal, mucosal	Immune, GBA	Naive CD8+ CD45RA+ intraepithelial lymphocytes and lamina propria lymphocytes negatively correlated with mucosal microbial diversity. Fecal microbial diversity negatively correlated with HADS
Pinto-Sanchez et al. 2017 ¹²⁷	44 IBS	BL [∞] vs. pcbo	Fecal	GBA, immune, urinary metabolites, neurotransmitters, and neurotrophins.	BL ↓depression and associated with ↓limbic reactivity. No difference in fecal microbiota, serum markers of inflammation, neurotrophins and neurotransmitters. Reduced urine methylamines and aromatic amino acids metabolites with BL.
Parthasarathy et al. 2017 ²¹⁷	25 CC, 25 HV	NA	Fecal	Transit	Reproducibility of fecal microbiota lower in normal transit vs. slow transit constipation
Parthasarathy et al. 2016 ¹⁵⁷	25 CC, 25 HV	NA	Fecal, mucosal	Transit	Fecal microbiota profile associated with colonic transit; genera from Firmicutes correlated with faster colonic transit.
Tian et al. 2017 ²¹⁸	60 STC	Fecal microbiota transplantation (FMT)	NA	Transit	FMT associated with faster transit vs. control treatment

Figure Legends:

Figure 1: Factors that shape the gut microbiota

Figure 2: Distribution of the gut microbiota within the gastrointestinal tract along its longitudinal and radial axes

Figure 3: Gut microbiota effects on host physiology including gastrointestinal motility, sensation, secretion, epithelial barrier integrity, immune activation, and brain-gut communication





